

Figure 1
Fatty Acid Biosynthetic Pathway

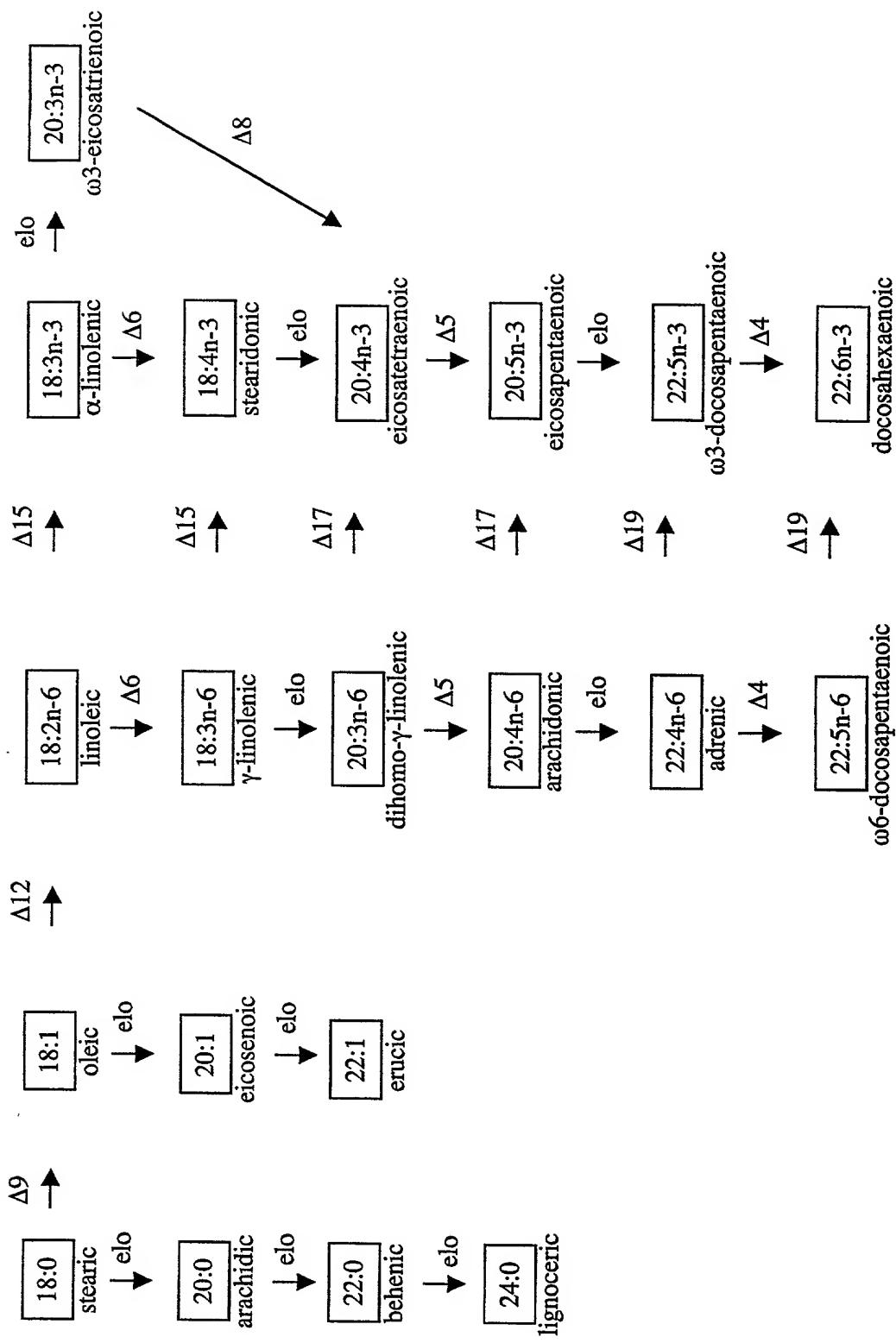


Figure 2

Gene Sequence of *sdd17*, an Omega-3 Fatty Acid Desaturase Gene
from *Saprolegnia diclina* (ATCC 56851)

1 ATGACTGAGG ATAAGACGAA GGTCGAGTTC CCGACGCTCA CGGAGCTCAA
51 GCACTCGATC CCGAACCGGT GCCTTGAGTC GAACCTCGGC CTCTCGCTCT
101 ACTACACGGC CCGCGCGATC TTCAACCGGT CGGCCTCGGC GGCGCTGCTC
151 TACGCCGGCGC GCTCGACGCC GTTCATTGCC GATAACGTTC TGCTCCACGC
201 GCTCGTTTGC GCCACCTACA TCTACGTGCA GGGCGTCATC TTCTGGGGCT
251 TCTTCACGGT CGGCCACGAC TGCAGGCCACT CGGCCTTCTC GCGCTACCAC
301 AGCGTCAACT TTATCATCGG CTGCATCATG CACTCTGCCA TTTTGACGCC
351 GTTCGAGAGC TGGCGCGTGA CGCACCGCCA CCACCACAAG AACACGGGCA
401 ACATTGATAA GGACGAGATC TTTTACCCGC ACCGGTCGGT CAAGGACCTC
451 CAGGACGTGC GCCAATGGGT CTACACGCTC GGCGGTGCGT GGTTTGTCTA
501 CTTGAAGGTC GGGTATGCC CGCGCACGAT GAGCCACTTT GACCCGTGGG
551 ACCCGCTCCT CCTTCGCCGC GCGTCGGCCG TCATCGTGT GCTCGGCCGTC
601 TGGGCCGCCT TCTTCGCCGC GTACCGTAC CTCACATACT CGCTCGGCTT
651 TGCCGTCACT GGCCTCTACT ACTATGCGCC GCTCTTGTC TTTGCTTCGT
701 TCCTCGTCAT TACGACCTTC TTGCACCAACA ACGACGAAGC GACGCCGTGG
751 TACGGCGACT CGGAGTGGAC GTACGTCAAG GGCAACCTCT CGAGCGTCGA
801 CCGCTCGTAC GGCGCGTTCG TGGACAAACCT GAGCCACAC ATTGGCACCG
851 ACCAGGTCCA CCACTTGTTC CCGATCATTC CGCACTACAA GCTCAACGAA
901 GCCACCAAGC ACTTTGCCGC CGCGTACCCG CACCTCGTGC GCAGGAACGA
951 CGAGCCCATC ATCACGGCCT TCTTCAAGAC CGCGCACCTC TTTGTCAACT
1001 ACGGCGCTGT GCCCGAGACG GCGCAGATCT TCACGCTCAA AGAGTCGGCC
1051 GCGGCCGCCA AGGCCAAGTC GGACTAA

Figure 3

Amino Acid Sequence of an Omega-3 Fatty Acid Desaturase (SDD17) from *Saprolegnia diclina* (ATCC 56851)

1 MTEDKTKVEF PTLTELKHSI PNACFESNLG LSLYYTARAI FNASASAALL
51 YAARSTPFIA DNVLLHALVC ATYIYVQGVI FWGFFTVGHD CGHSAFSRYH
101 SVNFIIGCIM HSAILTPFES WRVTHRHHHK NTGNIDKDEI FYPHRSVKDL
151 QDVRQWVYTL GGAWFVYLKV GYAPRTMSHF DPWDPLLLRR ASAVIDVSLGV
201 WAAFFAAYAY LTYSLGFAVM GLYYYAPLFV FASFLVITTF LHHNDEATPW
251 YGDSEWTYVK GNLSSVDRSY GAFVDNLSHH IGTHQVHHLF PIIPHVKLNE
301 ATKHFAAAYP HLVRRNDEPI ITAFFKTAHL FVNYGAVPET AQIFTLKESA
351 AAAKAKSD*

Figure 4

Comparative analysis of *S. diclina* Delta 17-desaturase (SDD17.pep) & *Synechocystis* sp. Delta 15-desaturase (SYCDESB)

Frame: 2 initn: 733 init1: 305 opt: 689 z-score: 996.8 expect(): 1.5e-47
40.9% identity in 269 aa overlap
(76-336:204-471)

	50	60	70	80	90	100
SDD17.pep	SAALLYAARSTPFIADNVLLHALVCATYIIVQGVIFWGFTVGHDCGHSAFSRYHNSVNF					
SYCDESB	YFFLDVGLIAGFYALAAYLDSWFFYPIFWLIIQGTILFWSLFFVGHDGCGHSFSKSKTLLNW					
	530	560	590	620	650	680
SDD17.pep	110	120	130	140	150	160
SYCDESB	IGCIMHSAILTTPFESWRVTHRHHHKNTGNIDKDEIFYPHRSVKDLO			DVRQWVYITLG		
	710	740	770	800	830	860
SDD17.pep	IGHLSHTPIILVPYHGWRISHRTHANTGNIDIDESWYPVSEOKYNQMAWEYKLLRFYLPL					
SYCDESB	170	180	190	200	210	220
SDD17.pep	GAWFVYLIKVGYAPRTMSHFDPWDPILL-RRASAVIVSLGWAAFFAAAYAYLTYISLGFAVM					
SYCDESB	IAYPIYLFRRRSPNROQSHFMPGSPLFRPGEKAAVLTSTFALAAYFGFLGFLIWQFGWLFL					
	890	920	950	980	1010	1040
SDD17.pep	230	240	250	260	270	280
SYCDESB	GLYYYYAPLFVFASFLVTTIFLHHNDEATPWYGDSEWTVVKGNLSSVDRSYGAFVDNLSHH					
	1070	1100	1130	1160	1190	1220
SDD17.pep	LKFYVAPYLVFVVWLDLVTFLHTEDNIPWYRGDDWYFLKGALSTIDRDYG-FINPIIHHD					
SYCDESB	290	300	310	320	330	
SDD17.pep	IGTHQVHHIFPIIPHYSKLNEATKHFAAAYPHLVRNRDEPIIITAFFKT			AHLFVNHYGAV		
SYCDESB	1250	1280	1310	1340	1370	1400
SDD17.pep	340	350				
SYCDESB	PETAQIFTLKESAAAAKAKSD					
SDD17.pep	VYYQSPSNNGGYQKKPXLILIESNQHREGROQYXMVLLPSDRLMRSMEEVKQSHSKRSALNO					
SYCDESB	1430	1460	1490	1520	1550	1580

Figure 5

Comparative analysis of *S. diclina* Delta 17-desaturase (SDD17.pep)
C. elegans Delta 17-desaturase (CELFAT)

Frame: 1 initn: 490 init1: 222 opt: 502 z-score: 724.0 expect(): 2.3e-32
 31.6% identity in 310 aa overlap
 (2-303:49-347)

		10	20	30	
SDD17.pep		MTEDEKTKVEFPPTLTELKHSTPNACFESNLGL			
		:: :::: : :: :::: :			
CELFAT	VTGGDVLDARASLEEKEAPRDVNANTKQATTEPRIQLPTVDAFRRAIPAHCFERDLVK				
		80 110 140 170 200 230			
SDD17.pep	SLYYTARAIFNASASAALLYAARSTPFIADNVLLHALVCATYIYVQGVIFWGFFTVGHD				
	: :: : : : : :: : :: :				
CELFAT	SIRYLVQDF——AALTILYFALPAFEYFGFLFGYLWNIFM——GVFGFALFVVGHD				
		260 290 320 350 380			
SDD17.pep	100 110 120 130 140				
	GHSAFSRYHSVNFIIIGCIMHSAILTPFESWRVTHRHHKNTGNIDKD—EIFYPHRSVKD				
	:: :: : :: : : : :: :: :: ::				
CELFAT	LHGSFSDNQNQLNDFIGHIAFSPLFSPYFPWQSHKLHHAFTNHIDKDGHVWIQDKDWEA				
	410 440 470 500 530 560				
SDD17.pep	150 160 170 180 190 200				
	LQDVRQWV——YTLLGGAWF-VYLKVGYAPRTMSHFDPWDPLLLRRASAVIVSLGVWA				
	: : :: : : : :: : :: :: ::				
CELFAT	MPSWKRFNPPIPFSGLKWFPVYTLFGFC—DGSHFWPYSSLFVRNSDRVQCVISGICCC				
	590 620 650 680 710 740				
SDD17.pep	210 220 230 240 250 260				
	FAAYAYLTYSLGFAVMGLYYYAPLFVFASFLVTTTFLHHNDEATPWYGDSEWTVKG				
	: :: :: : : : :: : :: ::				
CELFAT	VCAYTALTAGSYSNWFWYYWVPLSFFGLMLVITYLQHVDDVAEVYEADEWSFVRGOTC				
	770 800 830 860 890 920				
SDD17.pep	270 280 290 300 310 320				
	SVDRSYGAFVDNLSHHI-GTHQVHHLFPIIPHYKLNEATKHFAAAAYPHLVRRNDEPIITA				
	:: : : : : : : : : :				
CELFAT	TIDRYYGLGLDTTMHHITDGHVAHHFFNKIPHYHLLTEATEGVKKVLEPLSDTOQGYKSQV				
	950 980 1010 1040 1070 1100				
SDD17.pep	330 340 350				
	FFKTAHLFVNNGAVPETAQIFTLKESAAAAKAKSD				
CELFAT	NYDFFARFLWFNYKLDYLVLHKTAGIMQFRITLEEKAKAKXXKNIPCRSRVQQQLLRFHRFC				
	1130 1160 1190 1220 1250 1280				

Figure 6

Gene Sequence of *sdd12*, a Delta 12-Desaturase Gene
from *Saprolegnia diclina* (ATCC 56851)

1 ATGTGCAAAG GTCAAGCTCC TTCCAAGGCC GACGTGTTCC ACGCTGCGGG
51 GTACCGCCCG GTCGCCGGCA CGCCCGAGCC GCTGCCGCTG GAGCCCCCGA
101 CGATCACGCT CAAGGACCTG CGCGCGGCGA TCCC GGCCCA CTGCTTGAG
151 CGCAGCGCTG CCACTAGCTT TTACCATTTG GCCAAGAACC TTGCGATCTG
201 CGCCGGCGTG TTCGCCGTT GCCTCAAGCT CGCGGCTGCC GACTTGCCGC
251 TCGCGGCCAA GCTGGTCGCG TG GCCCATCT ACTGGTTCGT CCAGGGCACG
301 TACTTTACGG GCATCTGGGT CATTGCGCAC GAATGCGGCC ACCAGGCAGT
351 CTCGGCGTCC GAGATCCTCA ACGACACGGT CGGTATCATT CTTCACTCGC
401 TCCTCTTGT GCCGTACAC AGCTGGAAGA TCACGCCACCG CCGCCACCAC
451 TCCAACACGG GCAGCTGCGA GAACGACGAG GTGTTACGC CGACGCCGG
501 GTCCGTCGTC GAGGCCAAGC ACGACCAACTC GCTCCTCGAA GAGAGCCCCG
551 TCTACAACCT GTACGGCATC GTCATGATGC TTCTCGTGGG CTGGATGCCG
601 GGCTACCTCT TCTTCAACGC GACCGGCCCG ACCAAGTACG CTGGCCTCGC
651 CAAGTCGCAC TTCAACCCGT ACGCAGCCTT TTTCCCTCCA AAGGAGCGCC
701 TCAGCATCTG GTGGAGCGAC CTCTGCTTCC TCGCGGCCCTT GTACGGCTTT
751 GGCTACGGCG TCTCGGTCTT CGGCCTCCTC GATGTCGCCCG GCCACTACAT
801 CGTGCCGTAC CTCATTGCA ACGCGTACCT CGTGCATC ACgtACCTCC
851 AGCACACGGA TACGTACGT CCCCACTTCC CGGGCGACGA GTGGAACCTGG
901 CTGGCGGGCG CGCTCTGCAC CGTCGACCGC TCGTTGGCG CGTGGATCGA
951 CAGCGCGATC CACCACATTG CGCACACGCA CGTGACGCAC CACATTTCT
1001 CCAAGACGCC CTTCTACAC GCGATCGAGG CGACCGACGC CATCACGCC
1051 CTCCCTGGCA AGTACTACCT CATCGACCCG ACGCCGATCC CGCTGGCGCT
1101 CTGGCGCTCG TTCACGGACT GCAAGTACGT CGAGGACGAC GGCAACGTG
1151 TGTTTTACAA GCGCAAGCTC GAGGAAAAGT AA

Figure 7

Amino Acid Sequence of a Delta 12-Desaturase (SDD12) from *Saprolegnia diclina* (ATCC 56851)

1 MCKGQAPSKA DVFHAAAGYRP VAGTPEPLPL EPPTITLKDL RAAIPAHCFE
51 RSAATSFYHL AKNLAICAGV FAVGLKLAAA DLPLAAKLVA WPIYWVFVQGT
101 YFTGIWVIAH ECGHQAFSAS EILNDTVGII LHSLLFVPYH SWKITHRRHH
151 SNTGSCENDE VFTPTPRSVV EAKHDHSLLE ESPLYNLYGI VMMLLVGWMP
201 GYLFFNATGP TKYAGLAKSH FNPYAAFFLP KERLSIWWSD LCFLAALYGF
251 GYGVSVFGLL DVARHYIVPY LICNAYLVLI TYLQHTDTYV PHFRGDEWNW
301 LRGALCTVDR SFGAWIDSAY HHIADTHVTH HIFSKTPFYH AIEATDAITP
351 LLGKYYLIDP TPIPLALWRS FTHCKYVEDD GNVVFYKRKL EEK*

Figure 8

Comparative analysis of *S. diclina* Delta 12-desaturase (SDD12.pep)
 & *G. hirsutum* Delta 12-desaturase (GHO6DES)

Frame: 3 initn: 992 init1: 413 opt: 1086 z-score: 1531.8 expect(): 2.3e-77
 45.6% identity in 379 aa overlap
 (9-380:14-384)

SDD12.pep	10	20		30	40	
	MCKGQAPSKADVFHAAGYRPVAGTPEP			LPLEPPTITTLKDLRAAIPAH		
	: : : :	: : :		: : :	::	
GHO6DESAT	LRVSSTWRXTAFFKASKMAGGRMPIDGIKEENRGSVNRVPIEKPPFTLGQIKQAIPPHC					
	10	40	70	100	130	160
SDD12.pep	50	60	70	80	90	100
	FERSAATSFYHLAKNLAICAGVFAVGLKLAADLPLAAKLVAWPIYWFWQGITYFTGIWVI					
	: : :: : : : : : : : : : : :	: : : : : : : : :				
GHO6DESAT	FRRSLLRSFSYVVHDLCLASFFYYIATSYFHF-LPQPF SYIAWPVYWWLQGCILTGVVVI					
	190	220	250	280	310	340
SDD12.pep	110	120	130	140	150	160
	AHECGHQAFSASEILNDTVGIIILHSLLFVPYHSWKITHRRHHSNIGSCENDEVFTPTPRS					
	: : : : : : : : : :	: : : : : : : : : :				
GHO6DESAT	AHEWGHHAFRDYQWDDTVGLILHSALLVPYFSWKISHRRHHSNIGSMERDEVFPKPKS					
	370	400	430	460	490	520
SDD12.pep	170	180	190	200	210	220
	VVEAKHDHSILLESPLYNLGYIVMMLLVGWMPGYLFPNATGPTKYAGLAKSHFNPYAAFF					
	: : : : : : : : : : : :	: : : : : : : : :				
GHO6DESAT	KLSC—FAKYLNPPGRVLISLVTILTGW—PMYLAFNVSG—RYYDRILASHYNPYGPIY					
	550	580	610	640	670	
SDD12.pep	230	240	250	260	270	280
	LPKERLSIWWSDLICFLAALYGFYGVSVFGILLDVARHYIVPYLICNAYLVLITYLOHTDT					
	: : : : : : : : : : : :	: : : : : : : : : :				
GHO6DESAT	SDRERLQVYISDTGIFAVIYVLYKIAATKGLAWLLCTYGVPLLIVNAFLVLLITYLOHTHS					
	700	730	760	790	820	850
SDD12.pep	290	300	310	320	330	340
	YVPHFRGDEWNWLRGALCTVDRSGAWIDSAIHHIADTHVTHHIFS KTPFYHATEATDAI					
	: : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : :				
GHO6DESAT	ALPHYDSSEWDWLRGALSTM RDGFV-LNKVFHNITDTHVAHHLFSTM PHYHAMEATKAI					
	880	910	940	970	1000	1030
SDD12.pep	350	360	370	380	390	
	TPLLGKYYLIDPTPIPLALWRSFTHCKYVEDDGNNVVFYKRKLEEK					
	: : : : : : : : : : : : : :	: : : : : : : : : : : : : :				
GHO6DESAT	KPILGKYYFDGTPYKAMWREAKECLYVEPDVGGGGGGSKGVFWYRNKFXRPTNCLTAG					
	1060	1090	1120	1150	1180	1210
GHO6DESAT	RRNQRKTYLLDXCXIYGKLIINGRMWNSCLVVLCIKCCINKLYGRKKKK					
	1240	1270	1300	1330	1360	

Figure 9

Sequence ID:

Sequence ID 1

5'-ATC CGC GCC GCC ATC CCC AAG CAC TGC TGG GTC AAG-3'

Sequence ID 2

5'- GCC CTC TTC GTC CTC GGC CAY GAC TGC GGC CAY GGC TCG TTC TCG-
3'

Sequence ID 3

5'-GAG RTG GTA RTG GGG GAT CTG GGG GAA GAR RTG RTG GRY GAC RTG-3'

Sequence ID 4

5'-CCC TAC CAY GGC TGG CGC ATC TCG CAY CGC ACC CAY CAG AAC-3'

Sequence ID 5

5'-GTT CTG RTG RTG GGT CCG RTG CGA GAT GCG CCA GCC RTG GTA GGG-3'

Sequence ID 6

5'- GGC TCG CAC TTC SAC CCC KAC TCG GAC CTC TTC GTC-3'

Sequence ID 7

5'- GAC GAA GAG GTC CGA GTM GGG GTW GAA GTG CGA GCC-3'

Sequence ID 8

5'- GCG CTG GAK GGT GGT GAG GCC GGC GCG GAW GSA CGA CCA-3'

Sequence ID 9

5'- CTG GGG GAA GAG RTG RTG GAT GAC RTG GGT GCC GAT GTC RTG RTG-
3'

Sequence ID 10

5' - GGT GGC CTC GAY GAG RTG GTA RTG GGG GAT CTK GGG GAA GAR RTG-
3'

Sequence ID 11

5' -GAG RTG GTA RTG GGG GAT CTG GGG GAA GAR RTG RTG GRY GAC RTG-3'

Sequence ID 12

5' -TAC GCG TAC CTC ACG TAC TCG CTC G-3'

Sequence ID 13

5' -TTC TTG CAC CAC AAC GAC GAA GCG ACG-3'

Sequence ID 14

5' -GGA GTG GAC GTA CGT CAA GGG CAA C-3'

Sequence ID 15

5' -TCA AGG GCA ACC TCT CGA GCG TCG AC-3'

Sequence ID 16

5' -CCC AGT CAC GAC GTT GTA AAA CGA CGG CCA G-3'

Sequence ID 17

5' - AGC GGA TAA CAA TTT CAC ACA GGA AAC AGC -3'

Sequence ID 18

5' -GGT AAA AGA TCT CGT CCT TGT CGA TGT TGC-3'

Sequence ID 19

5' -GTC AAA GTG GCT CAT CGT GC-3'

Sequence ID 20

5' -CGA GCG AGT ACG TGA GGT ACG CGT AC-3'

Sequence ID 21

5' -TCA ACA GAA TTC ATG ACC GAG GAT AAG ACG AAG GTC GAG TTC CCG-3'

Sequence ID 22

5'-AAA AGA AAG CTT CGC TTC CTA GTC TTA GTC CGA CTT GGC CTT GGC-3'

Sequence ID 23

5'-TCA ACA AAG CTT ATG ACC GAG GAT AAG ACG AAG GTC GAG TTC
CCG-3'

Sequence ID 24

5'-AAA AGA GAA TTC CGC TTC CTA GTC TTA GTC CGA CTT GGC CTT
GGC-3'

Sequence ID 25

1 ATGACTGAGG ATAAGACGAA GGTCGAGTTC CCGACGCTCA CGGAGCTCAA
51 GCACTCGATC CCGAACCGCGT GCTTTGAGTC GAACCTCGGC CTCTCGCTCT
101 ACTACACGGC CCGCGCGATC TTCAACCGCGT CGGCCTCGGC GGCGCTGCTC
151 TACGCGGCGC GCTCGACGCC GTTCATTGCC GATAACGTT TGCTCCACGC
201 GCTCGTTGC GCCACCTACA TCTACGTGCA GGGCGTCATC TTCTGGGGCT
251 TCTTCACGGT CGGCCACGAC TGCGGCCACT CGGCCTTCTC GCGCTACCAC
301 AGCGTCAACT TTATCATCGG CTGCATCATG CACTCTGCGA TTTTGACGCC
351 GTTCGAGAGC TGGCGCGTGA CGCACCGCCA CCACCCACAAG AACACGGGCA
401 ACATTGATAA GGACGAGATC TTTTACCCGC ACCGGTCGGT CAAGGACCTC
451 CAGGACGTGC GCCAATGGGT CTACACGCTC GGCGGTGCGT GGTTGTCTA
501 CTTGAAGGTC GGGTATGCC CGCGCACGAT GAGCCACTT GACCCGTGGG
551 ACCCGCTCCT CCTTCGCCGC GCGTCGGCCG TCATCGTGT GCTCGCGTC
601 TGGGCCGCCT TCTTCGCCGC GTACCGTAC CTCACATACT CGCTCGGCTT
651 TGCCGTCATG GGCCTCTACT ACTATGCC GCTCTTGTC TTTGCTTCGT
701 TCCTCGTCAT TACGACCTTC TTGCACCACA ACGACGAAGC GACGCCGTGG
751 TACGGCGACT CGGAGTGGAC GTACGTCAAG GGCAACCTCT CGAGCGTCGA
801 CCGCTCGTAC GGCGCGTTG TGGACAACCT GAGCCACCAAC ATTGGCACGC
851 ACCAGGTCCA CCACTTGTTC CCGATCATTG CGCACTACAA GCTCAACGAA
901 GCCACCAAGC ACTTTGCGGC CGCGTACCCG CACCTCGTGC GCAGGAACGA
951 CGAGCCCCATC ATCACGGCCT TCTTCAAGAC CGCGCACCTC TTTGTCAACT
1001 ACGGCGCTGT GCCCGAGACG GCGCAGATCT TCACGCTCAA AGAGTCGGCC
1051 GCGGCCGCCA AGGCCAAGTC GGACTAA

Sequence ID 26

1 MTEDKTKVEF PTLTELKHSI PNACFESNLG LSLYYTARAI FNASASAALL
51 YAARSTPFIA DNVLLHALVC ATYIYVQGVI FWGFFTVGHD CGHSAFSRYH
101 SVNFIIGCIM HSAILTPFES WRVTHRHHHK NTGNIDKDEI FYPHRSVKDL
151 QDVRQWVYTL GGAWFVYLKV GYAPRTMSHF DPWDPLLLRR ASAIVIVSLGV
201 WAAFFAAYAY LTYSLGFAVM GLYYYAPLFV FASFLVITTF LHHNDEATPW
251 YGDSEWTYVK GNLSSVDRSY GAFVDNLSHH IGTHQVHHLF PIIPHVKLNE
301 ATKHFAAAYP HLVRRNDEPI ITAFFKTAHL FVNYGAVPET AQIFTLKESA
351 AAAKAKSD*

Sequence ID 27

1 ATGGCCCCGC AGACGGAGCT CCGCCAGCGC CACGCCGCCG TCGCCGAGAC
51 GCCGGTGGCC GGCAAGAAGG CCTTTACATG GCAGGAGGTC GCGCAGCACA
101 ACACGGCGGC CTCGGCCTGG ATCATTATCC GCGGCAAGGT CTACGACGTG
151 ACCGAGTGGG CCAACAAGCA CCCC GGCGGC CGCGAGATGG TGCTGCTGCA
201 CGCCGGTCGC GAGGCCACCG ACACGTTCGA CTCGTACCAC CCGTTCAAGCG
251 ACAAGGCCGA GTCGATCTTG ACAAGTATG AGATTGGCAC GTTCACGGGC
301 CCGTCCGAGT TTCCGACCTT CAAGCCGGAC ACGGGCTTCT ACAAGGAGTG
351 CCGCAAGCGC GTTGGCGAGT ACTTCAAGAA GAACAACCTC CATCCGCAGG
401 ACGGCTTCCC GGGCCTCTGG CGCATGATGG TCGTGTTCGC GGTCGCCGGC
451 CTCGCCTTGT ACGGCATGCA CTTTCGACT ATCTTGCGC TGCAGCTCGC
501 GGCGCGGGCG CTCTTGCG TCTGCCAGGC GCTGCCGCTG CTCCACGTCA
551 TGCACGACTC GTCGCACGCG TCGTACACCA ACATGCCGTT CTTCCATTAC
601 GTCGTCGGCC GCTTGCCAT GGACTGGTTT GCCGGCGGCT CGATGGTGTG
651 ATGGCTCAAC CAGCACGTCG TGGGCCACCA CATCTACACG AACGTCGCGG
701 GCTCGGACCC GGATCTTCCG GTCAACATGG ACGGCGACAT CCGCCGCATC
751 GTGAACCGCC AGGTGTTCCA GCCCATGTAC GCATTCCAGC ACATCTACCT
801 TCCGCCGCTC TATGGCGTGC TTGGCCTCAA GTTCCGCATC CAGGACTTCA
851 CCGACACGTT CGGCTCGCAC ACGAACGGCC CGATCCGCGT CAACCCGCAC
901 GCGCTCTCGA CGTGGATGGC CATGATCAGC TCCAAGTCGT TCTGGCCTT
951 CTACCGCGTG TACCTTCCGC TTGCCGTGCT CCAGATGCCC ATCAAGACGT
1001 ACCTTGCAT CTTCTCCTC GCCGAGTTG TCACGGGCTG GTACCTCGCG
1051 TTCAACTTCC AAGTAAGCCA TGTCTCGACC GAGTGGCGCT ACCCATGCGG
1101 CGACGAGGCC AAGATGGCGC TCCAGGACGA GTGGGCAGTC TCGCAGGTCA

1151 AGACGTCGGT CGACTACGCC CATGGCTCGT GGATGACGAC GTTCCTTGCC
1201 GGCAGCCTCA ACTACCAGGT CGTGCACCA TTGTTCCCCA GCGTGTGCA
1251 GTACCACTAC CCGGCGATCG CGCCCATCAT CGTCGACGTC TGCAAGGAGT
1301 ACAACATCAA GTACGCCATC TTGCGGGACT TTACGGCGGC GTTCGTTGCC
1351 CACTTGAAGC ACCTCCGCAA CATGGGCCAG CAGGGCATCG CCGCCACGAT
1401 CCACATGGGC TAA

Sequence ID 28

1 ATGGCAAACA GCAGCGTGTG GGATGATGTG GTGGGCCGCG TGGAGACCGG
51 CGTGGACCAAG 51 CGTGGACCAAG
101 TCCCGATGAT GGACGTGTCC ACCATGCTGG CATTGAGGT GGGATACATG
151 GCCATGCTGC TCTTCGGCAT CCCGATCATG AAGCAGATGG AGAACCTTT
201 TGAGCTCAAG ACCATCAAGC TCTTGACAAA CTTGTTCTC TTCGGACTTT
251 CCTTGTACAT GTGCGTGGAG ACCATCCGCC AGGCTATCCT CGGAGGCTAC
301 AAAGTGTGGAG GAAACGACAT GGAGAAGGGC AACGAGTCTC ATGCTCAGGG
351 CATGTCTCGC ATCGTGTACG TGTCTGCGT GTCCAAGGCA TACGAGTTCT
401 TGGATACCGC CATCATGATC CTTTGCAAGA AGTTCAACCA GGTTCCCTC
451 TTGCATGTGT ACCACCATGC CACCATTGTT GCCATCTGGT GGGCTATCGC
501 CAAGTACGCT CCAGGAGGTG ATGCGTACTT TTCAGTGATC CTCAACTCTT
551 TCGTGCACAC CGTCATGTAC GCATACTACT TCTTCTCCTC CCAAGGGTTC
601 GGGTTCTGTGA AGCCAATCAA GCCGTACATC ACCACCCTTC AGATGACCCA
651 GTTCATGGCA ATGCTTGTGC AGTCCTTGTGA CGACTACCTC TTCCCATGCG
701 ACTACCCACA GGCTCTTGTG CAGCTTCTTG GAGTGTACAT GATCACCTTG
751 CTTGCCCTCT TCGGCAACTT TTTGTGCAG AGCTATCTTA AAAAGCCAAA
801 AAAGAGCAAG ACCAACTAA

Sequence ID 29

1 MTVGFDETVT MDTVRNHNMP DDAWCAIHGT VYDITKFSKV HPGGDIIMLA
51 AGKEATILFE TYHIKGVPDA VLRKYKVGKL PQGKKGETSH MPTGLDSASY
101 YSWDSEFYRV LRERVAKKLA EPGLMQRARM ELWAKAIFLL AGFWGSLYAM
151 CVLDPHGGAM VAAVTLGVFA AFVGTCIQHD GSHGAFSKSR FMNKAAGWTL
201 DMIGASAMTW EMQHVLGHHP YTNLiemeng LAKVKGADVD PKKVDQESDP
251 DVFSTYPMLR LHPWHRQRFY HKFQHLYAPL IFGFMTINKV ISQDVGVVLR
301 KRLFQIDANC RYGSPWNVAR FWIMKLLTTL YMVALPMYMQ GPAQGLKLFF

351 MAHFTCGEVL ATMFIVNHI EGVSYASKDA VKGVMAPPRT VHGVTPMQVT
401 QKALSAEST KSDADKTTMI PLNDWAACQC QTSVNWAVGS WFWNHFSGGL
451 NHQIEHHCFP QNPHTVNVYI SGIVKETCEE YGVPYQAEIS LFSAYFKMLS
501 HLRTLGNEDL TAWST*

Sequence ID 30

5'-CCG SAG TTC ACS ATC AAG GAG ATC CGC GAS KSC ATC CCG GCC
CAC TGC TTC -3'

Sequence ID 31

5'-GRS CTT CTT GAK GTG GWM SGT GGC CTC CTC GGC GTG GTA GWR
CGG CAT-3'

Sequence ID 32

5'-CCS STC TAC TGG GCC TGC CAG GGT RTC GTC CTC ACS GGT GTC
TGG-3'

Sequence ID 33

5'-CCS STC TAC TGG ATC RYS CAG GGT RTC GTC KGY ACS GGT GTC
TGG-3'

Sequence ID 34

5'-GGC GTG GTA GTG CGG CAT SMM CGA GAA GAR GTG GTG GGC GAC
GTG-3'

Sequence ID 35

5'-CAC GTA CCT CCA GCA CAC GGA CAC CTA CG-3'

Sequence ID 36

5'- GAT CGA CAG CGC GAT CCA CCA CAT TGC-3'

Sequence ID 37

5'- CAA ATG GTA AAA GCT AGT GGC AGC GCT GC-3'

Sequence ID 38

5'-AGT ACG TGC CCT GGA CGA ACC AGT AGA TG-3'

Sequence ID 39

5'- TCA ACA GAA TTC ATG TGC AAA GGT CAA GCT CCT TCC AAG GCC
GAC GTG -3'

Sequence ID 40

5'- AAA AGA AAG CTT TTA CTT TTC CTC GAG CTT GCG CTT GTA AAA
CAC AAC-3'

Sequence ID 41

1 ATGTGCAAAG GTCAAGCTCC TTCCAAGGCC GACGTGTTCC ACGCTGCCGG
51 GTACCGCCCCG GTCGCCGGCA CGCCCGAGCC GCTGCCGCTG GAGCCCCCGA
101 CGATCACGCT CAAGGACCTG CGCGCGCGA TCCCGGCCCA CTGCTTGAG
151 CGCAGCGCTG CCACTAGCTT TTACCATTG GCCAAGAACC TTGCGATCTG
201 CGCCGGCGTG TTCGCCGTTG GCCTCAAGCT CGCGGCTGCC GACTTGCCGC
251 TCGCGGCCAA GCTGGTCGCG TGGCCCATCT ACTGGTTCGT CCAGGGCACG
301 TACTTACGG GCATCTGGGT CATTGCGCAC GAATGCGGCC ACCAGGCGTT
351 CTCGGCGTCC GAGATCCTCA ACGACACGGT CGGTATCATT CTTCACTCGC
401 TCCTCTTGTCG GCCGTACAC AGCTGGAAGA TCACGCACCG CCGCCACAC
451 TCCAACACGG GCAGCTGCGA GAACGACGAG GTGTTACGC CGACGCCGCG
501 GTCCGTGTC GAGGCCAACG ACGACCACTC GCTCCTCGAA GAGAGCCCGC
551 TCTACAACCT GTACGGCATC GTCATGATGC TTCTCGTGGG CTGGATGCCG
601 GGCTACCTCT TCTTCAACGC GACCGGCCCG ACCAAGTACG CTGGCCTCGC
651 CAAGTCGCAC TTCAACCCGT ACGCAGCCTT TTTCCTCCCA AAGGAGCGCC
701 TCAGCATCTG GTGGAGCGAC CTCTGCTTCC TCGCGGCCCTT GTACGGCTTT
751 GGCTACGGCG TCTCGGTCTT CGGCCTCCTC GATGTCGCCGCC GCACTACAT
801 CGTGCCTAC CTCATTGCA ACGCGTACCT CGTGCTCATC ACGTACCTCC
851 AGCACACGGA TACGTACGTG CCCCCACTTCC GCGGCGACGA GTGGAACCTGG
901 CTGCGCGCG CGCTCTGCAC CGTCGACCGC TCGTTCGCG CGTGGATCGA
951 CAGCGCGATC CACCACATTG CCGACACGCA CGTGACGCAC CACATTTCT
1001 CCAAGACGCC CTTCTACAC GCGATCGAGG CGACCGACGC CATCACGCC
1051 CTCCTCGGCA AGTACTACCT CATCGACCCG ACGCCGATCC CGCTGGCGCT
1101 CTGGCGCTCG TTCACGCACT GCAAGTACGT CGAGGACGAC GGCAACGTTG

1151 TGTTTACAA GCGCAAGCTC GAGGAAAAGT AA

Sequence ID 42

1 MCKGQAPSKA DVFHAGYRP VAGTPEPLPL EPPTITLKDL RAAIPAHCFE
51 RSAATSFYHL AKNLAI CAGV FAVGLKLAAA DLPLAA KLVA WPIYWVFVQGT
101 YFTGIWVIAH ECGHQAFSAS EILNDTVGII LHSLLFVPYH SWKITHRRHH
151 SNTGSCENDE VFTPTPRSVV EAKHDHSILLE ESPLYNLYGI VMMLLVGWMP
201 GYLFFNATGP TKYAGLAKSH FNPYAAFFLP KERLSIWWSD LCFLAALYGF
251 GYGVS VFGLL DVARHYIVPY LICNAYLVLI TYLQHTDTYV PHFRGDEWNW
301 LR GALCTVDR SFGAWIDS AII HHIADTHVTH HIFSKTPFYH AIEATDAITP
351 LLGKYYLIDP TPIPLALWRS FTHCKYVEDD GNVVFYKRKL EEK*